

Transgenic animal model for neurodegenerative diseases

The present invention relates to a mouse parkin2 DNA- and protein sequence containing naturally occurring or artificially introduced mutations or 5 deletions, which cause Parkinson's disease in a human if they occur in the according human sequence, the construction of a truncated parkin gene, which expresses no, a non-active or a truncated parkin protein and a model of a transgenic animal, expressing such a less or non-active parkin protein instead of the native parkin protein or no parkin protein, as well 10 as to the use of such a transgenic animal as a model for neurodegenerative diseases, preferred Parkinson's disease.

Neurodegenerative disorders are some of the most feared illnesses in society. During the last 10 years some of the genetic causes of many of 15 the primary neurodegenerative disorders like Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, prion disease and several ataxic syndromes, have been identified. These 1. findings gave new insights in the knowledge about the initiating trigger as well as the resulting consequences of those diseases. Due to the fact that 20 these diseases have many pathological mechanisms in common it seems possible that only relatively few pathways to neuronal death are involved in these disorders. Thus, treatment strategies for a particular neurodegenerative disease may be found to have value in other related disorders.

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Parkinson's disease is a progressive neurodegenerative movement disorder with severe symptoms like rigidity, bradykinesia or tremor. The disease symptoms appear after degeneration of more than 70-80% of dopaminergic neurons. Broadly speaking the disease falls into two categories, namely 30 late onset and early onset. Late onset, which occurs in older age (55+ years), mainly as consequence of environmental influences, leads to

enhanced dopaminergic neuron death at a faster rate and to a more severe degree than normal. Early onset Parkinson's disease is much more infrequent but starts between the ages of 35 and 60 years. There is evidence that three forms of this early type of Parkinson's disease show a 5 tendency to run in families and is therefore known as familial Parkinson's disease.

11 In both the early and late onset types of Parkinson's disease, the pathology is the same but the abnormalities tend to be more severe and 10 more widespread in cases beginning at an earlier age. The disease is characterised by lesions in brain areas where the cell bodies of the dopaminergic neurons are located mainly in the substantia nigra compacta. In addition intracytoplasmic inclusions known as Lewy bodies can be observed in different brain regions, in particular in substantia nigra and 15 the locus ceruleus.

Recently two loci could be identified associated with early onset PD, one on human chromosome 4q21-23 ("PARK 1" gene locus) with a gene defect to be due to a missense mutation in the α -synuclein protein (or *parkin1*), a 20 small abundant brain molecule (Polymeropoulos, M. et al., Science 1997; 276:2045-2047), and one on chromosome 2p13 ("PARK 3" gene locus) (Gasser, T. et al., Nat. Genet. 1998; 18: 262-265). Both forms are inherited in an autosomal dominant manner.

25 Lately an autosomal recessive form of familial Parkinson's disease could be observed, linked to human chromosome 6q25.2-27 ("PARK 2" gene locus) (Matsumine, H. et al., Am J Hum Genet (1997); 60: 588-596). This gene, designated *parkin* (or later *parkin2*) contains 12 exons spanning more than 500 kb and encodes a protein of 465 amino acids (molecular weight 51,652 30 Dalton) with homology to ubiquitin at the N-terminal portion and a RING-finger like motif at the C-terminal portion.

It has been shown, that mutations in the α -synuclein gene lead to autosomal dominant Parkinson's disease (Polymeropoulos, M. *et al.*, Science 1997; 276: 2045-2047), as well as mutations in the parkin gene cause autosomal recessive juvenile parkinsonism (Kitada, T. *et al.*, Nature 1998; 392: 605-608; Hattori, N. *et al.*, Biochem Biophys Res Comm 1998; 249: 754-758)).

Further Hattori, N. *et al.*, have been shown in Ann Neurol 1998; 44: 935-941, that different deletions in the parkin gene are the reason for 10 truncated parkin proteins, causing autosomal recessive juvenile parkinsonism. Especially intragenic deletional mutations, involving exons 3 to 4, exon 3, exon 4 and exon 5, as well as exon 3 through exon 7 are described as effecting the disease. Deletion of exon 3 of the parkin gene is furthermore described by Lücking, C. *et al.* in the Lancet 1998; 352: 15 1355-1356 to cause autosomal recessive juvenile parkinsonism.

Investigations of Abbas, N. *et al.* Human Molecular Genetics 1999; 8: 567-574 and Kitada, T. *et al.*, Nature 1998; 392: 805-808 show that mutations in the ubiquitin-like N-terminal part (exon 2) of the parkin gene can also cause autosomal recessive juvenile parkinsonism, as well as different 20 frameshift- or missense mutations.

Leroy, E. *et al.*, demonstrated in Hum Genet 1998; 103: 424-427 that 25 deletions of exons 5, 6 and 7 of the human parkin gene leads to early onset Parkinson's disease.

At present most common therapies are dealing with the increase of dopamine content in PD patients via application of L-dopa as precursor of dopamine, dopamine agonists or MAO-B (Monoamino Oxidase B) inhibitors, e.g. Deprenyl, by blocking the degradation of dopamine. There are no prophylactic therapies available to stop the progression of the degenerative 30 disease before onset of symptoms in late onset PD. This is due to the fact that at present diagnosis is only possible when first symptoms occur. So

far it is not clear to which extent genetic components enhance the environmental components responsible for the increased cell death of dopaminergic neurons.

5 Although different transgenic animal models for neurodegenerative diseases like Alzheimer's disease have been created, a transgenic animal model for Parkinson's disease has not yet been described.

Homologous recombination may be employed for inactivation or alteration of 10 genes in a site-directed manner. A number of papers describe the use of homologous recombination in mammalian cells, including human cells. Illustrative of these papers are Kucherlapati *et al.* (1984) Proc. Natl. Acad. Sci. USA 81:3153-3157; Kucherlapati *et al.* (1985) Mol. Cell. Bio. 5:714-720; Smithies *et al.* (1985) Nature 317:230-234; Wake *et al.* (1985) 15 Mol. Cell. Bio. 8:2080-2089; Ayares *et al.* (1985) Genetics 111:375-388; Ayares *et al.* (1986) Mol. Cell. Bio. 7:1656-1662; Song *et al.* (1987) Proc. Natl. Acad. Sci. USA 84:6820-6824; Thomas *et al.* (1986) Cell 44:419-428; Thomas and Capecchi (1987) Cell 51:503-512; Nandi *et al.* (1988) Proc. Natl. Acad. Sci. USA 85:3845-3849; and Mansour *et al.* (1988) Nature 20 336:348-352. Various aspects of using homologous recombination to create specific genetic mutations in embryonic stem cells and to transfer these mutations to the germline have been described (Evans and Kaufman (1981) Nature 294:154-146; Dotschman *et al.*, (1987) Nature 330:576-578; Thomas and Capecchi (1987) Cell 51:503-512; Thompson *et al.* (1989) Cell 56:316-25 321. The combination of a mutant polyoma enhancer and a thymidine kinase promoter to drive the neomycin gene has been shown to be active in both embryonic stem cells and EC cells by Thomas and Capecchi, *supra*, 1987; Nicholas and Berg (1983) in *Teratocarcinoma Stem Cell*, eds. Siver, martin and Strikland (Cold Spring Harbor Lab., Cold Spring Harbor, N.Y. (pp. 469-30 497); and Linney and Donerly, Cell 35:693-699, 1983.

The object of the present application is to provide the suppositions for a test model for neurodegenerative diseases, preferably Parkinson's disease and a valuable tool in the diagnosis and treatment of these conditions, as well as the development of experimental models of Parkinson's disease that

5 can be used to define further the underlying biochemical events involved in the pathogenesis of this disease.

This object is met by a polynucleotide sequence encoding a mouse parkin2 protein, containing naturally occurring or artificially introduced

10 mutations or deletions, which cause Parkinson's disease in a human if they occur in the according human sequence, a vector, containing such a sequence, a prokaryotic or eukaryotic cell, containing such a vector and a transgenic non-human animal, whose one or both alleles of a gene encoding a parkin gene are mutated in a way, that a protein with modified,

15 preferred less activity or no active protein is expressed.

The transgenic non-human animals according to the present invention can be

11 used as models for analysing the symptoms of neurodegenerative diseases or as a model system for testing the efficacy of a treatment for a neuro-

20 degenerative disease, whereby it is not an object of the present application to provide any method for treating one of the described diseases in a human or animal.

Such models could presumably be employed, in one application, to screen

25 for agents that alter the degenerative course of Parkinson's disease. For example, a model system of Parkinson's disease could be used to screen for environmental factors that induce or accelerate the pathogenesis. Further an experimental model could be used to screen for agents that inhibit, prevent, or reverse the progression of Parkinson's disease. Presumably,

30 such models could be employed to develop pharmaceuticals that are effective in preventing, arresting, or reversing Parkinson's disease. Further such models can be used for examination of behaviour during the

development of a neurodegenerative disease, for examination of physiological and molecular biological correlation of the disease, for studies of drug effects and for determination of effective drug doses and toxicity. These applications should be considered as examples and should 5 not limit the application of the models in any way.

The present invention provides model systems of neurodegenerative diseases, preferred Parkinson's disease, wherein the model system comprises a mutated isoform or a fragment of the mouse parkin2 gene 10 (further designated as *mPark2*), a DNA sequence derived from SEQ ID NO: 1 encoding a mouse parkin2 protein corresponding to the human parkin protein encoded by human chromosome gene region 6q25.2-27 ("PARK 2" gene locus). Preferred the model system contains a mutated *mPark2* sequence or a *mPark2* sequence containing any deletion, coding for a mutated or truncated, less 15 active or non-active parkin protein.

The sequence of human α -synuclein (*parkin1*) gene, as well as human parkin (*parkin2*) gene is known. Human parkin2 gene (further designated as *hPark2*) contains 12 exons, coding for a protein which has in full length 465 amino 20 acids and a molecular weight of 51,652 Daltons.

The present application shows the full length cDNA of *mPark2* in SEQ ID NO:1, consisting of 12 exons, containing the full length open reading frame for the mouse parkin2 protein (SEQ ID NO:4) which coding region 25 consists of 1395 bp, coding for a protein of 464 amino acids with a calculated molecular weight of 51615 Dalton. Further two shorter cDNAs spanning a coding region of 789 bp (SEQ ID NO: 2 (isolated from mouse brain cDNA library by specific PCR)) and 753 bp (SEQ ID NO: 3 (isolated from mouse kidney cDNA library by specific PCR)) corresponding to amino 30 acid sequences of 262 amino acids (SEQ ID NO:5) and 250 amino acids (SEQ ID NO:6) respectively are provided.

During the work of isolation and sequencing of the sequences SEQ ID NO: 1 to 3 shown in this application Shimizu, N. et al. submitted a mouse parkin DNA sequence to the EMBL GenBank database, published in July 1999 with the accession number AB019558. The protein sequence of the mouse parkin 5 protein encoded by the published sequence is identical to SEQ ID No: 4.

The present invention refers to polynucleic acid sequences derived from SEQ ID NO: 1, containing naturally occurring or artificially introduced mutations or deletions, which are known to cause Parkinson's disease in a 10 human if they occur in the according human sequence.

The present invention encompasses further polynucleotide sequences containing naturally occurring mutations according to the wobble principle, which represents the degeneration of the genetical code, as 15 well as according to the polymorphism of the genetical code, encoding any protein which has the same or a homologous amino acid sequence as any of the mutated or truncated mouse parkin2 proteins of the present invention.

“Homologous amino acid sequence” in content with the mouse parkin2 protein 20 means in the present application an amino acid sequence, wherein at least 70 %, preferably 80 %, more preferably 90 % of the amino acids are identical to one of the proteins of the present invention and wherein the replaced amino acids preferably are replaced by homologous amino acids. As “homologous” amino acids are designated which have similar features 25 concerning hydrophobicity, charge, steric features etc. Most preferred are amino acid sequences, containing the species-dependent differences of the mouse amino acid sequence compared to human parkin protein shown in the alignment Figure No. 1. The alignment of the corresponding polynucleotide sequences with the exon boundaries is shown in Figure No. 2.

In the whole application for nucleotides and amino acids the usual designations (one-letter ~~are~~ three-letter code) are used, known by any person skilled in the art.

5 The full length polynucleotide sequence of SEQ ID NO:1 or fragments thereof can be obtained by isolation of genomic DNA, containing exons and introns of the mPark2 gene, by RNA transcripts of the DNA or by the preparation of cDNA, containing only the exons of the mPark2 gene. Further the full length sequence as well as fragments thereof may be obtained by
10 synthetical polymerisation of nucleotides.

A preferred polynucleotide sequence of the present application is a polynucleotide sequence derived from SEQ ID NO: 1, which is either mutated or in which parts of the sequence are deleted. Mutations, insertions or
15 deletions may be located 5'upstream of the open reading frame (i.e. in the promotor-region), or they can concern one or more exons of the open reading frame. More preferred is a sequence, containing either a mutated full length sequence or fragments of SEQ ID NO:1, encoding a truncated parkin2 protein (i.e. by mutations leading to a STOP codon or by
20 deletions) or no protein (i.e. if the mutation or deletion is located in the promoter-region in exon 1).

More preferred mutations or deletions concern either exon 1, wherein the promotor region is contained, or exon 3 and/or one or more of the other
25 exons.

Most preferred the polynucleotide sequence of the present application is selected from SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID
30 NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17; SEQ ID NO: 18, SEQ ID NO:19 or SEQ ID NO:20 (see also Table 1 and 2).

One of the polynucleotide sequences SEQ ID NO:1 to 3 may be treated *in vitro* or *in vivo* by random or site-directed mutagenesis, by random or site-directed digestion, by recombination or fusion or any other method known of persons skilled in the art to obtain sequences derived from SEQ 5 ID NO:1 containing mutations or deletions leading to a less active or to no parkin protein. Of course a person skilled in the art will understand that the present invention encompasses as well any construction in which parts of or the whole polynucleotide sequence encoding the parkin gene is deleted or replaced by another sequence (i.e. by a sequence encoding an 10 antibioticum-resistance).

To obtain at least a transgenic non-human animal as a model for neurodegenerative diseases, the natural occurring sequence of the parkin gene in this animal may be replaced on one or both alleles of the 15 chromosomes by a sequence of mPark2, containing mutations or deletions according to the present invention. These animals produce either less or less active or no parkin protein.

The transgenic animals of the present invention are created using targeted 20 gene replacement, a sequence by which a specific DNA sequence of interest (target DNA) is replaced by an altered DNA (replacement DNA). The genome of embryonic stem (ES) cells is modified using homologous recombination (Capecchi, Science 1989; 244:1288 and U.S. Pat. No. 5,487,992). The embryonic stem cells are injected in blastocysts as an early state of the 25 developing embryo. The blastocysts are then placed in a pseudopregnant female animal.

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Briefly, a vector is constructed that carries the replacement DNA. Both 30 ends of the replacement DNA are flanked by long DNA sequences homologous to the sequences flanking the target DNA. When the vector is introduced into ES cells, the homologous sequences align and recombination may take place. This results in the target DNA being exchanged for the replacement

1 DNA. The vector is not replicated in the cells, and will be lost. The frequency of homologous recombination is low; thus, a screening system is used. The replacement DNA will contain a positive marker sequence, usually a neomycin resistance gene. Thus, any cells that incorporate the 5 replacement DNA by homologous recombination will resist neomycin. By growing cells in medium containing the drug neomycin one can select only those cells containing the replacement DNA. The ES cells containing the replacement DNA are then inserted into recipient mouse blastocysts to create chimeric mice. Chimeras with germ cells derived for the altered ES 10 cells transmit the modified genome to their offspring, yielding mice heterozygous for the target DNA (contain one target DNA and one replacement DNA). The heterozygotes are then bred with each other either to create mice homozygous for the replacement DNA and deficient in the target DNA or to maintain transgenic heterozygotes if the homozygotic mice 15 are not viable.

The DNA will comprise at least a portion of the gene(s) at the particular locus with introduction of a lesion into at least one, usually both 20 copies, of the native gene(s), so as to prevent expression of a functional parkin protein. The lesion may be an insertion, deletion, replacement or combination thereof. When the lesion is introduced into only one copy of the gene being inactivated, the (heterozygote) cells having a single unmutated copy of the target gene are amplified and may be subjected to a second transformation, where the lesion may be the same or different from 25 the first lesion, usually different, and where a deletion, or replacement is involved, may be overlapping at least a portion of the lesion originally introduced. The resulting transformants are screened for the absence of the functional protein of interest and the DNA of the cell may be further screened to ensure the absence of a wild-type target gene. 30 Alternatively, homozygosity as to a phenotype may be achieved by breeding hosts heterozygous for the mutation.

For the construction of a transgenic animal model according to the present application any suitable animal may be employed, however mammals are preferred. More preferred are rodents and most preferred are rats and mice.

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In the following the single steps of creating the animal models will be described in detail.

Starting from a polynucleotide sequence encoding a parkin gene, preferably 10 from a sequence encoding a mPark2 gene, more preferably from a sequence according to any of SEQ ID NO:1 to 3, most preferred from SEQ ID NO: 1 a desired mutation, insertion or deletion is introduced to the sequence.

Methods to create mutations by random or site-directed mutagenesis or desired insertions or deletions by random or site-directed digestion 15 and/or replacement are commonly known to persons skilled in the art and broadly described in the literature. The method how a mutation, insertion or deletion is introduced in the sequence is not relevant, however falls under the scope of the present invention, as long as any of the later described nucleotides, amino acids or sequences are involved.

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The constructs may be modified to include functional entities other than the mutated sequence which may find use in the preparation of the construct, amplification, transformation of the host cell, and integration of the construct into the host cell.

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The homologous sequence for targeting the construct may have one or more deletions, insertions, substitutions or combinations thereof. For example, the mPark2 gene may include a deletion at one site and an insertion at another site which includes a gene which may be used for selection, where 30 the presence of the inserted gene will result in a defective inactive protein product. Preferably, substitutions are employed. For an inserted gene, of particular interest is a gene which provides a marker, e.g.,

antibiotic resistance such as neomycin resistance, including G418 resistance.

The deletion will be at least about 50 bp, or more usually at least about

5 100 bp, and generally not more than about 20 kbp, where the deletion will normally include at least a portion of the coding region including a portion of or one or more exons, a portion of one or more introns, and may or may not include a portion of the flanking non-coding regions, particularly the 5'-non-coding region (transcriptional regulatory region).

10 Thus, the homologous region may extend beyond the coding region into the 5'-non-coding region or alternatively into the 3'-non-coding region. Insertions will generally not exceed 10 kbp, usually not exceed 5 kbp, generally being at least 50 bp, more usually at least 200 bp.

15 The homologous sequence should include at least about 100 bp, preferably at least about 150 bp, more preferably at least about 300 bp of the target sequence and generally not exceeding 20 kbp, usually not exceeding 10 kbp, preferably less than about a total of 5 kbp, usually having at least about 50 bp on opposite sides of the insertion and/or the deletion in order to

20 provide for double crossover recombination.

Upstream and/or downstream from the target gene construct may be a gene which provides a tool to select out primary random integration of the construct in the genome. For this purpose, the herpes simplex virus

25 thymidine kinase gene may be employed, since the presence of the thymidine kinase gene may be detected by the use of nucleoside analogs, such as Gancyclovir or Acyclovir, for their cytotoxic effects on cells that contain a functional HSV-tk gene. The absence of sensitivity to these nucleoside analogs indicates that homologous recombination has occurred.

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The presence of the marker gene inserted into the gene of interest establishes the integration of the target construct into the host genome.

However, DNA analysis might be required in order to establish whether homologous or non-homologous recombination occurred. This can be determined by employing probes for the insert and then sequencing the 5' and 3' regions flanking the insert for the presence of the gene of 5 interest extending beyond the flanking regions of the construct or identifying the presence of a deletion, when such deletion is introduced.

The polymerase chain reaction (PCR) may be used, with advantage in detecting the presence of homologous recombination (Kim and Smithies, 10 (1988) Nucleic Acid Res. 16:8887-8903; and Joyner et al (1989) Nature 338:153-156). Primers may be used which are complementary to a sequence within the construct, usually complementary to the selection marker gene, and complementary to a sequence outside the construct and at the target locus. In this way, one can only obtain DNA duplexes having both of the 15 primers present in the complementary chains in homologous recombination has occurred. By demonstrating the presence of the primer sequences or the expected size sequence, the occurrence of homologous recombination is supported. Any person skilled in the art knows how to determine the suitable PCR primers and conditions.

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The construct may further include a replication system which is functional in the mammalian host cell. For the most part, these replication systems will involve viral replication systems, such as Simian Virus 40, Epstein-Barr virus, papilloma virus, adenovirus and the like.

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Where a marker gene is involved, as an insert, and/or flanking gene, depending upon the nature of the gene, it may have the wild-type transcriptional regulatory regions, particularly the transcriptional initiation regulatory region or a different transcriptional initiation 30 region. Whenever a gene is from a host where the transcriptional initiation region is not recognized by the transcriptional machinery of the mammalian host cell, a different transcriptional initiation region

will be required. This region may be constitutive or inducible, preferably inducible. A wide variety of transcriptional initiation regions have been isolated and used with different genes. Of particular interest as promoters are the promoters of metallothionein-I and II from a mammalian host, thymidine kinase, beta-actin, immunoglobulin promoter, human cytomegalovirus promoters, and SV40 promoters. In addition to the promoter, the wild-type enhancer may be present or an enhancer from a different gene may be joined to the promoter region.

- 5 10 The construct may further include a replication system for prokaryotes, particularly *E. coli*, for use in preparing the construct, cloning after each manipulation, allowing for analysis, such as restriction mapping or sequencing, followed by expansion of a clone and isolation of the plasmid for further manipulation. When necessary, a different marker may be
- 15 employed for detecting bacterial transformants.

Once the vector has been prepared, it may be further manipulated by deletion of the bacterial sequences as well as linearisation, where a short deletion may be provided in the homologous sequence, generally not 20 exceeding about 500 bp, generally being from about 50 to 300 bp. The small deletion will generally be near one or other end of the targeted structural gene.

The construction of the desired polynucleotide sequence may be carried out 25 in a cloning vector and linearised prior to the transfection of ES cells. A broad range of cloning vectors as well as vectors for the homologous recombination are commercially available and may be selected according to the desired construction.

- 30 Cloning vectors are usually replicated in prokaryotic cells, which renders the selection and multiplication of the desired construct. It is not

critical which prokaryotic organism is used, but usually *E.coli* or a yeast strain is preferred.

E. coli is one prokaryotic host useful particularly for cloning the DNA 5 sequences of the present invention. Other microbial hosts suitable for use include bacilli, such as *Bacillus subtilis*, and other enterobacteriaceae, such as *Salmonella*, *Serratia*, and various *Pseudomonas* species. In these prokaryotic hosts, one can also make expression vectors, which will typically contain expression control sequences compatible with the host 10 cell (e.g., an origin of replication). In addition, any number of a variety of well-known promoters will be present, such as the lactose promoter system, a tryptophan (trp) promoter system, a beta-lactamase promoter system, or a promoter system from phage lambda. The promoters will typically control expression, optionally with an operator sequence, 15 and have ribosome binding site sequences and the like, for initiating and completing transcription and translation.

Other microbes, such as yeast, may also be used for expression.

Saccharomyces is a preferred host, with suitable vectors having expression 20 control sequences, such as promoters, including 3-phosphoglycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired.

Homologous recombination may be used to insert a mutant sequence into a 25 host genome at a specific site, for example, at a host parkin locus. In one type of homologous recombination, one or more host sequence(s) are replaced; for example, a host parkin allele (or portion thereof) is replaced with a mutant parkin allele (or portion thereof). In addition to such gene replacement methods, homologous recombination may be used to 30 target a mutant parkin allele to a specific site other than a host parkin locus. Homologous recombination may be used to produce transgenic non-human animals and/or cells that incorporate mutant parkin alleles.

Further to the above described techniques a step of expressing the treated sequence may be inserted in the expiration. Therefore the construct is (sub)cloned into any expression vector, which may be brought into a 5 suitable eukaryotic cell. These expression vectors are typically replicable in the host organisms either as episomes or as an integral part of the host chromosomal DNA. Commonly, expression vectors will contain selection markers, e.g., tetracycline resistance or hygromycin resistance, to permit detection and/or selection of those cells transformed with the 10 desired DNA sequences. Polynucleotides encoding a variant parkin2 polypeptide may include sequences that facilitate transcription (expression sequences) and translation of the coding sequences, such that the encoded polypeptide product is produced. Construction of such polynucleotides is well known in the art and is described further in 15 Maniatis et al. Molecular Cloning: A Laboratory Manual, 2nd Ed. (1989), Cold Spring Harbor, N.Y. For example, but not for limitation, such polynucleotides can include a promoter, a transcription termination site (polyadenylation site in eukaryotic expression hosts), a ribosome binding site, and, optionally, an enhancer for use in eukaryotic expression hosts, 20 and, optionally, sequences necessary for replication of a vector.

Any suitable eukaryotic cell may be used, but insect cells or mammalian cells as primary cells or immortalized cell lines are preferred.

25 A number of suitable host cell lines capable of secreting intact human proteins have been developed in the art, and include the CHO cell lines, various COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Baculovirus expression systems are useful for high level expression of heterologous genes in eukaryotic cells. Knops et al. (1991) J. Biol. Chem. 30 266(11):7285. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter, an enhancer (Queen et al. (1986) Immunol. Rev. 89:49, and necessary

processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites, and transcriptional terminator sequences. Preferred expression control sequences are promoters derived from immunoglobulin genes, SV40, Adenovirus, Bovine Papilloma Virus, and the like. The vectors containing the DNA segments of interest can be transferred into the host cell by well-known methods, which vary depending on the type of cellular host. For example, calcium chloride transfection is commonly utilized for prokaryotic cells, whereas calcium phosphate treatment, microinjection of DNA into the nucleus or electroporation may be used for other cellular hosts. (See, generally, Maniatis, et al. Molecular Cloning: A Laboratory Manual, 2nd. Ed. Cold Spring Harbor Press, (1989). The DNA may be single or double stranded, linear or circular, relaxed or supercoiled DNA. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology (1990) 185:527-537.

For the creation of an animal model according to the present invention each polynucleotide sequence can be used, containing mutations, insertions or deletions which are known to cause Parkinson's disease in a human, when they occur in the corresponding human sequence. Preferred polynucleotide sequences for the creation of an animal model according to the present invention are those which mutations are shown in table 2. More preferred are polynucleotide sequences containing mutations or deletions shown in table 1. The most preferred polynucleotide sequence for the construction of a transgenic animal of the present invention is SEQ ID NO: 7. Further enclosed to the present invention is an animal model wherein the parkin sequence is replaced by an according sequence of another mammal (i.e. by the human sequence, containing one of the mutations, insertions or deletions described in the present application) or by a sequence encoding a marker, i.e. an antibioticum.

Table 1: Mutations or deletions in mPark2 cDNA (SEQ ID NO:1)

Position in SEQ ID NO:1	Replacement (DNA)	Replacement (protein)	SEQ ID NO (DNA seq)	SEQ ID NO (prot seq)
NT 300-540	Exon3	Frameshift, Truncation	7	21
NT 300-659	Exon3-4	ORF, deletion of 121 aa	8	22
NT 300-996	Exon3-7	Frameshift, Truncation	9	23
NT 541-659	Exon 4	Frameshift, Truncation	10	24
NT 659-744	Exon 5	Frameshift, Truncation	11	25
NT 660-996	Exon 5-7	Frameshift, Truncation	12	26
NT 996-1208	Exon 8-9	Frameshift, Truncation	13	27
NT: 229-230 (aa 34)	deletion AG	Gln→Stop at aa 38, nonsense	14	28
NT: 282 (aa 52)	deletion A	Asn→Stop at aa 54, nonsense	15	29
NT: 350-351 (aa 74)	deletion AG	Arg→Stop at aa 78, nonsense	16	30
NT: 136-299	Exon 2	Frameshift, Truncation	17	31

aa = amino acid

NT = nucleotide

Table 2: Replaced amino acids in mPark2 cDNA (SEQ ID NO:1)

Position in SEQ ID NO:1	Replacement (DNA)	Replacement (protein)	SEQ ID NO (DNA seq)	SEQ ID NO (prot seq)
NT: 608	G→T,	Lys→Asn (aa 161)	18	32
NT: 1369	C→A,	Thr→Asn (aa 415)	19	33
NT: 1483	G→A,	Trp→Stop (aa 453)	20	34

aa = amino acid

5 NT = nucleotide

Once the construct has been prepared and manipulated, the DNA is isolated from the prokaryotic host according to any method known in the art. Before the DNA construct is introduced into the target cells for homologous

10 recombination undesired sequences may be removed from the vector, e.g. the undesired bacterial sequences. As target cells an embryonic stem (ES) cell line may be used. As already indicated above for the expression system, any convenient technique for introducing the DNA into the target cells may be employed. After transformation of the target cells, many target cells
15 are selected by means of positive and/or negative markers, as previously indicated, neomycin resistance and Acyclovir or Gancyclovir resistance. Those cells which show the desired phenotype may then be further analyzed by restriction analysis, electrophoresis, Southern analysis, polymerase chain reaction or the like. By identifying fragments which show the
20 presence of the lesion(s) at the target gene site, one can identify cells in which homologous recombination has occurred to inactivate the target gene.

For embryonic stem cells, after mutation, the cells may be plated onto a
25 feeder layer in an appropriate medium, e.g., fetal bovine serum enhanced DMEM. Cells containing the construct may be detected by employing a selective medium and after sufficient time for colonies to grow, colonies

may be picked and analyzed for the occurrence of homologous recombination. As described previously, the polymerase chain reaction may be used, with primers within and without the construct sequence but at the target locus. Those colonies which show homologous recombination may then be used for 5 embryo manipulating by blastocyst injection. Blastocysts may be obtained from 4 to 6 week old superovulated females by flushing the uterus 3.5 days after ovulation. The embryonic stem cells may then be trypsinized and the modified cells added to a droplet containing the blastocysts. At least one, usually at least about 10, and up to about 15 of the modified 10 embryonic stem cells may be injected into the blastocoel of the blastocyst. After injection, at least one and not more than about 15 of the blastocysts are returned to each uterine horn of pseudopregnant females. Alternatively, any of the common techniques, i.g. microinjection of the mutated gene, or a fragment thereof, into a one-cell embryo 15 followed by incubation in a foster mother can be used.

~~Consequently, the animals will be born 16-18 days after introduction of the mutated gene into the blastocysts.~~
~~The pups will usually be born 16-18 days after introduction of the~~
~~blastocysts into foster mothers. Chimeric animals will be mated with wild~~
~~type (wt) mice to create heterozygote transgenics.~~

20 With these methods it is possible to obtain transgenic non-human animals, whose one or both alleles of a gene encoding a parkin gene are mutated in a way, that a parkin protein with modified, preferred less activity or no active parkin protein is expressed.

25 "Mutated" means in this context replacements, insertions or deletions of nucleotides or polynucleotide sequences.

30 In consequence of the mutated parkin gene these animals produce a mutated or truncated parkin protein or no parkin protein. Preferred - if a parkin protein is expressed - the parkin protein expressed by the transgenic animal contains any of the mutations or deletions shown in table 1 and 2,

represented by any of the proteins with an amino acid sequence of SEQ ID NO:5, SEQ ID NO:6, SEQ, ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34 or naturally occurring or artificially introduced mutants with a homologous protein sequence or fragments thereof, particularly preferred a parkin protein with a sequence according to SEQ ID NO:21 is expressed.

The expression of one of these proteins or no parkin protein in the transgenic non-human animals causes these animals to display features of a neurodegenerative disease. These features can be manifested in developing physiological, biochemical or molecular biological modifications in e.g. cells, tissues, organs or neuronal structures.

In accordance with standard protocols, cultured eukaryotic cells, either primary cultures or immortalised cell lines, may be transfected, either transiently or stably, with a mutant or fragmented mPark2 allele so that the cultured eukaryotic cell expresses a mutant parkin2 polypeptide.

The present application further refers to cells, typically mammalian cells and preferably mammalian cells of the neural, glial, or astrocytic lineage, that have been transformed or transfected with any DNA sequence according to the present invention, as well as to any cells which have been derived from a transgenic non-human animal, whereby the cells express any of the mutated parkin2 proteins isoforms according to the present invention, preferred any of the isoforms shown in table 1 or 2 or fragments thereof, or they contain a parkin sequence which is mutated in a way that they don't express a parkin protein. The cells derived from the transgenic animals may be cultured as cell-lines or as primary cultures.

Once established, all such cell lines can be grown continuously in culture and may be used for a variety of in vitro experiments to study parkin expression and processing.

- 5 The present invention further refers to a method of producing transgenic non-human animals and transformed cells that contain any polynucleotide sequence encoding any mutant mouse parkin2 protein isoform according to the present invention, preferably such as shown in table 1 or 2 or naturally occurring or artificially introduced mutants or fragments
- 10 thereof.
- 15 Preferred, the above described polynucleotide sequences, the proteins and amino acid sequences as well as the transgenic animal models and cell lines may be used for any method for analysing the symptoms of neurodegenerative diseases.

Such neurodegenerative diseases encompass among others Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multisystem atrophy, Wilson's disease, Pick's disease, Prion disease, or second causes inducing Parkinson's syndromes like toxins (e.g. Mn, Fe, 6-hydroxydopamine, MPTP (1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine), CO), drugs, brain tumors, head trauma, stroke, vascular irregularities, or metabolic irregularities.

- 25 Enclosed to these methods are methods outside of a living body, which are methods of molecular biology like PCR, Southern and Northern blot analysis, construction of DNA or RNA probes, as well as Western blot analysis, preparation of epitopes from the protein or amino acid sequences mentioned in this application, production of monoclonal and polyclonal
- 30 antibodies. These methods may be used for screening of samples, preferred of biological fluids for either the expression of parkin protein as a method for detecting the presence of the protein, or in a nucleic acid

sample or another sample removed from a subject, the presence of the gene for Parkinson's disease comprising identifying a genetic alteration in a gene sequence coding for parkin. Further enclosed are pathobiochemical, immunobiological and neurological as well as histochemical methods carried out after sacrificing the animal for considering the effects of neurodegenerative diseases, particularly Parkinson's disease to the living body. Further methods for locating the presence of genetic alterations associated with Parkinson's disease are provided. These methods may be used outside of a living body to predict the development of the disease prior to onset or for genetic screening.

However, particularly preferred is a method of testing the efficacy of a treatment for a neurodegenerative disease associated with a less active or non-active parkin protein, comprising subjecting any of the created transgenic animals as a model to a putative treatment and determining the efficacy of said treatment.

These testing methods preferably comprise administering an active substance, whose effect can be determined by any of the above described methods, to a transgenic animal according to the present invention.

By the use of the transgenic animals described in the present application it is possible the first time to test in a model system whether an active substance is useful for treating a condition associated with non-active parkin protein and determining a level of the active substance, which causes an effect in treating the disease.

Treatments may carried out as single dose applications, but it is preferred to use the transgenic animals in long-time experiments with multiple dose applications.

The transgenic animals of the present application may be particularly used as model systems for screening for drugs and evaluating drug effectiveness. Additionally, such model systems provide a tool for defining the underlying biochemistry of neurodegenerative diseases, which

5 thereby provides a basis for rational drug design. The models may be used further for studies of behaviour, physiological and molecular biological examinations, pharmacological and toxicological studies and several other applications.

10 Having detected the genetic mutation in the gene sequence coding for parkin protein in an individual not yet showing overt signs of Parkinson's disease, using any of the methods of the present invention, it may be possible to employ gene therapy, in the form of gene implants, to prevent the development of the disease.

15 Additional embodiments directed to modulation of the production of variant parkin proteins include methods that employ specific antisense polynucleotides complementary to all or part of a variant parkin sequence according to any of the sequences mentioned in this application, or for

20 some embodiments a wild-type parkin sequence. Such complementary antisense polynucleotides may include nucleotide substitutions, additions, deletions, or transpositions, so long as specific hybridisation to the relevant target sequence is retained as a property of the polynucleotide. Thus, an antisense polynucleotide must preferentially bind to a variant

25 parkin sequence as compared to a wild-type parkin. It is mostly preferred that the antisense polynucleotide reflects the exact nucleotide sequence of the variant allele (or wild-type allele where desired) and not a degenerate sequence.

30 Complementary antisense polynucleotides include soluble antisense RNA or DNA oligonucleotides which can hybridise specifically to a variant parkin mRNA species and prevent transcription of the mRNA species and/or

translation of the encoded polypeptide (Ching et al. (1989) Proc. Natl. Acad. Sci. U.S.A. 86:10006; Broder et al. (1990) Ann. Int. Med. 113:604; Loreau et al. (1990) FEBS Letters 274:53-56); Holcenberg et al. W091/11535; U.S. Pat. No. 7,530,165 ("New human CRIPTO gene"--publicly 5 available through Derwent Publications Ltd., Rochdale House, 128 Theobalds Road, London, UK); W091/09865; W091/04753; W090/13641; and EP 386563, each of which is incorporated herein by reference). The antisense polynucleotides therefore inhibit production of the variant parkin polypeptides.

10

Antisense polynucleotides may be produced from a heterologous expression cassette in a transfectant cell or transgenic cell or animal, such as a transgenic neural, glial, or astrocytic cell, preferably where the expression cassette contains a sequence that promotes cell-type specific 15 expression (Wirak et al. loc. cit.). Alternatively, the antisense polynucleotides may comprise soluble oligonucleotides that are administered to the external milieu, either in the culture medium *in vitro* or in the circulatory system or interstitial fluid *in vivo*. Soluble antisense polynucleotides present in the external milieu have been shown 20 to gain access to the cytoplasm and inhibit translation of specific mRNA species. In some embodiments the antisense polynucleotides comprise methylphosphonate moieties. For general methods relating to antisense polynucleotides, see *Antisense RNA and DNA*, (1988), D. A. Melton, Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.).

25

Legends to the figures:

Figure 1 shows the alignment of the deduced amino acid sequences of the human and mouse Parkin2 protein (SEQ ID NO: 4).
30 Underlined are the conserved ubiquitin like (at the N-terminus) and Ring finger like (at the C-terminus) regions of both proteins.

Figure 2 shows the alignment of the nucleotide sequences of the human and mouse parkin 2 gene. Bold lines represent the exon boundaries identified for the human and mouse sequence.

5 Figure 3 represents a flow chart of the cloning procedure of the mouse parkin2 gene - exon3 knock-out construct.

Abbreviations:

a) Restriction endonucleases:

N = NotI, E = Eco RI, B = BamHI, H = HindIII, X = XbaI.

10 b) Modifications: () = T4 DNA polymerase treatment in order to remove a restriction site in the resulting plasmid.

c)  = pBluescript KSII (Stratagene) vector sequence
 = λ-Fix vector sequence

d) HSV-tk = Herpes simplex promoter and thymidine kinase gene

15 e) kb = kilobases

The following examples are provided for illustration and are not intended to limit the invention to the specific example provided.

20 Example 1

Isolation of mouse Parkin2 cDNA clones:

25 Arrayed mouse brain and mouse kidney cDNA libraries (Biofrontera Pharmaceuticals/ Bio Systems) were screened by PCR under standard conditions using the primers Ex2s: *tcaggttcaactccagctatggc* and Ex2as: *tgcctgcggaaatcacacgcagc*. The cycle conditions were the following: 3 min. 95°C, (30sec. 95°C, 30sec. 56°C, 1min. 72°C) x 35 cycles.

Single colonies containing the mPark2 genes were verified by colony hybridisation according to the protocol described by Maniatis *et al.* 1989 (see above).

5 Construction of the Del Exon3 parkin gene (according to SEQ ID NO: 7)

All the further described cloning steps are shown in Figure 3. A genomic lambda ZIP clone (genomic mouse λ -Fix library, Stratagene) containing the exon 3 of the parkin gene was isolated by PCR using exon3 specific primer 10 of the mPark2 gene. A 3.1 kb BamHI/HindIII fragment of the lambda ZIP clone containing genomic DNA 3' end to the exon3 of mPark2 was cloned into the cloning vector pBluescript KS (Stratagene) to obtain the plasmid pmPark2-BH. Secondly, a 5 kb HindIII/EcoRI genomic DNA fragment was inserted into the HindIII site of the pmPark2-BH-clone. The EcoRI and 15 HindIII sites were destroyed by T4 DNA polymerase treatment. As result the plasmid pmPark2-BE- with a 8.1 kb long genomic region to the 3'-end of the exon 3 could be obtained.

A 2.0 kb XbaI/XhoI (the XbaI restriction site is located within the 20 multiple cloning sequence (mcs) of Lambda Fix) genomic DNA fragment containing the genomic region 5' to the exon3 was cloned into the EcoRI site of the pNeoloxp-vector (Giese *et al.* Science, 1998, 279:870-3) after generation of blunt ends by T4 DNA polymerase treatment. The BamHI-site (5'-to the EcoRI-site) of this vector was used subsequently for the 25 insertion of the 2.5 kb HSV-tk-marker gene. Again T4 DNA polymerase was used to generate blunt ends before ligation in order to eliminate the used cloning site. The resulting vector was digested with the restriction enzymes NotI and XhoI to obtain a 6.5 kb fragment containing the HSV-tk, the 2kb XhoI/XbaI genomic region to 5'-end of exon3, and the neo-marker. 30 The vector pmPark2-BE was digested with XhoI to linearise the plasmid. Both the isolated 6.5 kb fragment as well as the linear vector were

treated with T4 DNA polymerase prior to ligation to eliminate the used restriction sites.

This plasmid pmPark2del-ex3 was linearised with the restriction enzyme

5 NotI prior to transfection into ES cells.

Example 2

Transfection of ES cells:

10

Isolation and Freezing of the ES cells:

14 days old embryos were isolated, head and organs were removed from

embryos, the remaining tissue was minced, and washed with 1x PBS. 1x

trypsin (0.5g/l) / EDTA (0.2g/l) was used for dissolve the tissue by

15 incubating them at 37°C for 5 min. The reaction was stopped by adding 1 vol. EF medium (Embryonic Feeder medium: 1x DMEM, 10% FCS Serum, 2mM

Glutamine, all obtained from LIFE Technologies), and cells were dissolved

by pipetting several time up and down. The supernatant was centrifuged

with 1000 rpm for 5 min. The fibroblasts from one embryo were seeded into

20 a 175 cm² flask with 30 ml medium. The medium was changed after 24 h. When

the fibroblasts form a confluent monolayer they were splitted 1:3, and

thereafter they were frozen when the cells are confluent again. Cells from

175 cm² flask were frozen into one tube. Therefore first empty tubes are

place on ice, freezing medium is added (EF medium + 20% DMSO

25 (Dimethylsulfoxid)), cells with 0.5 ml EF medium are added, mixed, putted

in a styrofoam box, which is cooled down in a -80°C freezer, and the next

day the tubes are transferred into liquid N₂(l) tank.

Sub-culturing, inactivation and feeder layer:

30 The fibroblasts can be cultured on gelatine-coated plastic ware. The cells

were splitted carefully 1:3 after 3 days. When feeder layer are needed for

ES cell culturing, the fibroblasts should be division-inactivated by

mitomycin C. 2 mg mitomycin C are dissolved in 10 ml PBS, which can be stored at -20°C. This stock solution is diluted 1:20 with EF medium for inactivation; the nearly confluent fibroblasts in a 175 cm² flask are incubated in 20-30 ml of medium with mitomycin C for 2 h at 37°C.

- 5 Mitomycin C is then removed by 2x washing with PBS, and the inactivated fibroblasts are recovered in EF medium for 24 h before they are frozen or used for ES cell culturing after a few days. The cells are stored 37°C until they are used (maximally 10 days;) or they are frozen. For feeder layer, plate cells onto the same area; here the plastic ware has to be
- 10 coated by gelatine.

Sub-culturing the ES-cells:

The ES cells were kept for 2-4 passages in culture. The medium is ES medium (1x DMEM, 15% FCS Serum, 2mM Glutamine, 1x nonessential amino acids, 7µl β Mercaptoethanol, with supplement containing LIF (Leukemia Inhibitory Factor, 2.5×10^5 to 10^6 U/l), all obtained from LIFE Technologies), and the cells are splitted 1:6 every second day. Cells were refeeded 2 h before passaging.

20 Stable Transfection of ES Cells

After digestion of the gene targeting construct the DNA is extracted with phenol/CHCl₃ (24/23) and precipitated with EtOH (wash 2x with 75% EtOH); the rest of EtOH is removed carefully and air dried for approx. 15 min under steril conditions (laminar flow). The DNA is suspended in H₂O (final conc.: 3 mg/ml). 5x10⁷ cells of a monolayer are treated with 1x trypsin to detach them from the ground of the flask, suspended in 0.8 ml medium and electroporated with DNA (30 µg linear DNA, 800 V, 3 µF, BioRad Gene Pulser). After 20 min at 4°C, cells are diluted with 9.5 ml medium and are plated onto dishes (9 cm diameter). 24 h after electroporation G418 (150-175 mg /ml) is added to start selection. The medium is changed every day; after 7-9 days of selection colonies can be picked.

Picking colonies and culturing of picked colonies:

24 colonies were picked with Eppendorf tips under an inverted microscope.

The colonies were transferred into the wells of a 96-well plate (round

bottom), 30 μ l 1xtrypsin/EDTA are added, and the plates are incubated 10

5 min at 37°C. Thereafter 100 μ l ES-medium are added and the cells are

suspended by pipetting up and down 12x with a multichannel pipette. The

trypsinized cells are solitarily plated into a 24-well plate. The medium

is exchanged every 24 h. 3-4 days after picking the cells are detached

from the ground of the plates. Therefore the medium is removed, 60 μ l

10 1xtrypsin/EDTA are added and the plates are incubated for 7 min at 37°C.

The treatment is stopped by adding 200 μ l medium and the cells are

resuspended. 200 μ l of the cell suspension is added to 200 ml medium with

20 % DMSO and the cells are frozen as described above.

15 Example 3

DNA isolation and southern blot analysis for control and identification of
picked colonies:

To characterize the clones, picked in example 2, DNA is isolated from the

20 cells and examined. Therefore 500 μ l medium are added into any well of a
picked colony which should still contain 60 μ l cell suspension (see

example 2). The cells are cultured continuously 3-4 days until confluent

for DNA isolation. 500 μ l lysis buffer (12 ml 1 M Tris-HCl (pH 8.3); 1.2

ml 0.5 M EDTA; 2.4 ml 10 % SDS; 4.8 ml 5 M NaCl; 1.2 ml 10 mg/ml

25 proteinase K; 98.4 ml H₂O) is added, and it is incubated over night at

55°C. DNA is precipitated by adding 1 vol. 2-propanol and at least 15 min

shaking at RT, and transferred with an Eppendorf tip into a 1.5 ml tube

with 1 ml 70% EtOH. The tube is centrifuged for 10 min at RT to spin down

the DNA. EtOH is removed and pellets are air dried for least one hour. DNA

30 is dissolved afterward in 100 μ l TE for over night at 55°C.

Southern blot analysis:

1/3 of the isolated DNA was used for one digestion. The digestion was carried out for over night at 37°C. Loading buffer was added, and DNAs are separated in an agarose gel for least 6 hours. The gels were incubated in 0.2 N HCl for 15 min at room temperature; after 15 min HCl solution was replaced by 0.4 N NaOH and the gel was incubated therein for 15 min at RT. The DNA was transferred onto nylon membranes (Amersham) over night using 0.4 N NaOH as transfer buffer using a vacuum blot machine (Stratagene). The membranes were neutralized in 2x SSC for 1 min, and air dried for least one hour. After UV-Crosslinking the DNA onto the membrane hybridisation with DNA probes (probes are shown in figure 3) was carried out under standard conditions (QuickHyb from Clontech, 65°C, wash twice with 2x SSC, 0.1 % SDS at 65°C).

Production of transgenic animals with mutant parkin allele:

15 10-15 recombinant ES cells are injected into blastocysts. The blastocysts are implanted in pseudopregnant mice. The chimeric spring offs are crossed with wild type mice to obtain heterozygotic recombinant F1 mice. These mice are analysed by southern blot analysis as described above. Transgenic 20 mice are crossed with each other to obtain mice with both alleles modified (homozygote animals).

25 Descendants of the transgenic animals may be used for breeding with mice strains representing the same or any other genotype, preferred mice strains showing neurological abnormalities, more preferred with strains showing neurodegenerative abnormalities. These other mouse strains may be selected from wild type mice, mice containing knock-ins or knock-outs, mice containing mutants of genes or mice which overexpress any gene product. The most preferred partners for breeding are mice which represent 30 a model for Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multisystem atrophy, Wilson's disease, Pick's disease or Prion disease.

Use of Transgenic Mice:

The animal can be used to test potential therapeutic agents. The test
5 group of mice is treated with the test compound administered in an appropriate fashion for a set period. At the conclusion of the test period, the animals are assessed behaviourally, biochemically, and histologically for any possible effects of the test compound. The exact protocol depends on the anticipated mechanism of action of the test
10 compound. Compounds that may have utility in treating Parkinson's disease can be identified using this approach.

Such analysis can be carried out in the animal, in primary tissue cultures of the expressing cells or in immortalised cells derived from those
15 animals.

Mice expressing the truncated parkin2 protein gene or variants of the described one can be used for testing the development of Parkinson's disease during ageing of the animals. Beside the enhanced progression of
20 cell death in substantia nigra area, increased sensitivity to selective neurotoxins like MPTP or 6-hydroxydopamine and enhanced response to dopaminergic precursors like L-dopa may be examined.